

# SEQUENCE LISTING

<110> McCall, Catherine A.  
Hunter, Shirley Wu  
Weber, Eric R.

<120> NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
AND USES THEREOF

<130> AL-2-C4

<140> not yet assigned

<141> 2000-09-14

<150> 09/292,225

<151> 1999-04-15

<150> 60/098,909

<151> 1998-09-02

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<170> PatentIn Ver. 2.1

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Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Ile Gln Ser Val Leu		
	130 135	140
Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu		
	145 150	155 160
Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr		
	165 170	175
Leu Ala Leu Val Arg Glu Leu Lys Asp Ala Phe Glu Pro His Gly Tyr		
	180 185	190
Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Arg Ala		
	195 200	205
Tyr Asp Ile Lys Glu Leu Asn Lys Leu Phe Asp Trp Met Asn Val Met		
	210 215	220
Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Phe Tyr Gly His Asn Ala		
	225 230	235 240
Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe		
	245 250	255
Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg		
	260 265	270
Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile		
	275 280	285
Glu Asp Arg Ser Lys Leu Lys Leu Gly Asp Pro Ala Lys Gly Met Ser		
	290 295	300
Pro Pro Gly Phe Ile Ser Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu		

305		310		315		320
Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu						
	325			330		335
Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr						
	340			345		350
Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu						
	355			360		365
Gly Val Ser Gly Val Met Val Trp Ser Leu Glu Asn Asp Asp Phe Lys						
	370			375		380
Gly His Cys Gly Pro Lys Asn Pro Leu Leu Asn Lys Val His Asn Met						
	385			390		400
Ile Asn Gly Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser						
	405			410		415
Thr Thr Thr Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr						
	420			425		430
Pro Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr						
	435			440		445
Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser						
	450			455		460
Pro Thr Thr Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser						
	465			470		475
						480
Thr Pro Ser Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr						
	485			490		495
Thr Thr Tyr Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp						
	500			505		510
Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val						
	515			520		525
Asn Gly Gly Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile						
	530			535		540
Trp Cys Gln Glu Lys Leu Thr Cys Ile Gly Glu						
	545			550		555



<210> 19  
 <211> 1665  
 <212> DNA  
 <213> Dermatophagoides farinae

<400> 19  
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 atgaaccac cagccaccat taacaaattc acagaccaa tatttgtgta tattggttgg 120  
 atgtgggata tcaccttctt tgtaacattt gataagatgt ccatcgacat aggttgtata 180  
 ttttgggtgt tcgcttgtgt gttcgggtcgt ggttggcgaa ggtgtcgatg ttgtaggggc 240  
 tgggtgttgg gttgttgggt ttggtgtggt gggagaagga gttgttgcg gtgtgggtggg 300  
 agaaggggtt gttgtcgggg tgggtgggaga aggggttgtt gtcgggggtgg tgggagaagg 360  
 agttgttggc gttgtatgcg ggggttgtggg tgtcgtcgtt ggagttgggtg tcgttgtact 420  
 tggacccaaa atgcattcga aagagttctt ttcacgcca ttaatcatat tatgaacttt 480  
 gttcaacaat ggatttttcg gtccgcagtg acctttgaaa tcatcatttt ccaatgacca 540  
 aaccatgaca ccagaaacgc ctaattcttt caggaaagcc aacttgcattg atatactggc 600  
 cagatcatcg taaccgaccc agattttatc attgtaacca tatggagcat tgtaatatct 660  
 atcgtattgg atatgccatt cttctttttg aaacaattga cacaattcta tatatgagag 720  
 gacaccttct tcaccagaaa tgaaacctgg gggcgacatg ctttgggtg gatctccaag 780  
 tttgagtttg cttcgatctt caatgctcca agcacggcca tagaatggaa caccattac 840  
 caatttgtct ctggtggcac cattgttcaa ataatagtgc atggtgtagt tgacattgaa 900  
 gtaagtgtgc aactcatcag tttcatctgg tcgtttatac aacggagcat tgtgaccgta 960  
 aaagttttcc catccaccgt ggtaatcata tgcatgaca ttcattcaat cgaacaattt 1020  
 gttcaattct ttgatatacat aagctcggtc gattttgtct ttacctggtg atactgcagc 1080  
 agtcaacaag tagccatgag gttcaaaagc gtctttaagt tctctaacca aagccaaata 1140  
 gttttgttta tcgattttcg ggtaaccaa tcgagatcca ggatactccc aatccaaatc 1200  
 tagaccgtcg aacttgtatt cttgcaaaaa gtccaaaact gattgtatga attgttgacg 1260  
 atatgttggg tttgcagcca tatcggaata tttttcggag cttcatacc aaccaccaag 1320  
 tgaaatcatg gtggttaatt ctggattctt caatcgcaag ttgttgaaac gttcataacc 1380  
 acgtttttcc catgagttat gggtatcatc ttggtaagga tcgaaaactt gaattgtgta 1440  
 tttgtattca tcaatttttag cgaaaccata cattaaatgt gtacacttga atggatcaat 1500  
 atcttcgata gtgtatggat caactttatg atatacggac catgttccaa cataacaaac 1560  
 aattctcatc ggatttttcg aataatcatt atgatctcgt ttgatggatg cattcataag 1620  
 gccaatgcag gccataatac taagtattgc atatatgggt ttcatt 1665

<210> 20  
 <211> 1608  
 <212> DNA  
 <213> Dermatophagoides farinae

<220>  
 <221> CDS  
 <222> (1)..(1608)

<400> 20  
 tcc atc aaa cga gat cat aat gat tat tcg aaa aat ccg atg aga att 48

Ser	Ile	Lys	Arg	Asp	His	Asn	Asp	Tyr	Ser	Lys	Asn	Pro	Met	Arg	Ile	
1				5				10						15		
gtt	tgt	tat	gtt	gga	aca	tgg	tcc	gta	tat	cat	aaa	gtt	gat	cca	tac	96
Val	Cys	Tyr	Val	Gly	Thr	Trp	Ser	Val	Tyr	His	Lys	Val	Asp	Pro	Tyr	
			20				25					30				
act	atc	gaa	gat	att	gat	cca	ttc	aag	tgt	aca	cat	tta	atg	tat	ggg	144
Thr	Ile	Glu	Asp	Ile	Asp	Pro	Phe	Lys	Cys	Thr	His	Leu	Met	Tyr	Gly	
			35				40					45				
ttc	gct	aaa	att	gat	gaa	tac	aaa	tac	aca	att	caa	gtt	ttc	gat	cct	192
Phe	Ala	Lys	Ile	Asp	Glu	Tyr	Lys	Tyr	Thr	Ile	Gln	Val	Phe	Asp	Pro	
			50				55					60				
tac	caa	gat	gat	aac	cat	aac	tca	tgg	gaa	aaa	cgt	ggg	tat	gaa	cgt	240
Tyr	Gln	Asp	Asp	Asn	His	Asn	Ser	Trp	Glu	Lys	Arg	Gly	Tyr	Glu	Arg	
			65			70				75					80	
ttc	aac	aac	ttg	cga	ttg	aag	aat	cca	gaa	tta	acc	acc	atg	att	tca	288
Phe	Asn	Asn	Leu	Arg	Leu	Lys	Asn	Pro	Glu	Leu	Thr	Thr	Met	Ile	Ser	
				85				90						95		
ctt	ggg	ggg	tgg	tat	gaa	ggc	tcg	gaa	aaa	tat	tcc	gat	atg	gct	gca	336
Leu	Gly	Gly	Trp	Tyr	Glu	Gly	Ser	Glu	Lys	Tyr	Ser	Asp	Met	Ala	Ala	
			100				105					110				
aat	cca	aca	tat	cgt	caa	caa	ttc	ata	caa	tca	gtt	ttg	gac	ttt	ttg	384
Asn	Pro	Thr	Tyr	Arg	Gln	Gln	Phe	Ile	Gln	Ser	Val	Leu	Asp	Phe	Leu	
			115				120					125				
caa	gaa	tac	aag	ttc	gac	ggg	cta	gat	ttg	gat	tgg	gag	tat	cct	gga	432
Gln	Glu	Tyr	Lys	Phe	Asp	Gly	Leu	Asp	Leu	Asp	Trp	Glu	Tyr	Pro	Gly	
			130			135					140					
tct	cga	ttg	ggg	aac	ccg	aaa	atc	gat	aaa	caa	aac	tat	ttg	gct	ttg	480
Ser	Arg	Leu	Gly	Asn	Pro	Lys	Ile	Asp	Lys	Gln	Asn	Tyr	Leu	Ala	Leu	
			145			150				155					160	
gtt	aga	gaa	ctt	aaa	gac	gct	ttt	gaa	cct	cat	ggc	tac	ttg	ttg	act	528
Val	Arg	Glu	Leu	Lys	Asp	Ala	Phe	Glu	Pro	His	Gly	Tyr	Leu	Leu	Thr	
			165					170					175			
gct	gca	gta	tca	cca	ggg	aaa	gac	aaa	atc	gac	cga	gct	tat	gat	atc	576
Ala	Ala	Val	Ser	Pro	Gly	Lys	Asp	Lys	Ile	Asp	Arg	Ala	Tyr	Asp	Ile	
			180				185					190				
aaa	gaa	ttg	aac	aaa	ttg	ttc	gat	tgg	atg	aat	gtc	atg	aca	tat	gat	624

Lys	Glu	Leu	Asn	Lys	Leu	Phe	Asp	Trp	Met	Asn	Val	Met	Thr	Tyr	Asp	
		195					200					205				
tac	cac	ggt	gga	tgg	gaa	aac	ttt	tac	ggt	cac	aat	gct	ccg	ttg	tat	672
Tyr	His	Gly	Gly	Trp	Glu	Asn	Phe	Tyr	Gly	His	Asn	Ala	Pro	Leu	Tyr	
	210					215					220					
aaa	cga	cca	gat	gaa	act	gat	gag	ttg	cac	act	tac	ttc	aat	gtc	aac	720
Lys	Arg	Pro	Asp	Glu	Thr	Asp	Glu	Leu	His	Thr	Tyr	Phe	Asn	Val	Asn	
	225				230					235				240		
tac	acc	atg	cac	tat	tat	ttg	aac	aat	ggt	gcc	acc	aga	gac	aaa	ttg	768
Tyr	Thr	Met	His	Tyr	Tyr	Leu	Asn	Asn	Gly	Ala	Thr	Arg	Asp	Lys	Leu	
				245					250					255		
gta	atg	ggt	gtt	cca	ttc	tat	ggc	cgt	gct	tgg	agc	att	gaa	gat	cga	816
Val	Met	Gly	Val	Pro	Phe	Tyr	Gly	Arg	Ala	Trp	Ser	Ile	Glu	Asp	Arg	
			260					265					270			
agc	aaa	ctc	aaa	ctt	gga	gat	cca	gcc	aaa	ggc	atg	tcg	ccc	cca	ggt	864
Ser	Lys	Leu	Lys	Leu	Gly	Asp	Pro	Ala	Lys	Gly	Met	Ser	Pro	Pro	Gly	
		275					280					285				
ttc	att	tct	ggt	gaa	gaa	ggt	gtc	ctc	tca	tat	ata	gaa	ttg	tgt	caa	912
Phe	Ile	Ser	Gly	Glu	Glu	Gly	Val	Leu	Ser	Tyr	Ile	Glu	Leu	Cys	Gln	
	290					295					300					
ttg	ttt	caa	aaa	gaa	gaa	tgg	cat	atc	caa	tac	gat	gaa	tat	tac	aat	960
Leu	Phe	Gln	Lys	Glu	Glu	Trp	His	Ile	Gln	Tyr	Asp	Glu	Tyr	Tyr	Asn	
	305				310					315					320	
gct	cca	tat	ggt	tac	aat	gat	aaa	atc	tgg	gtc	ggt	tac	gat	gat	ctg	1008
Ala	Pro	Tyr	Gly	Tyr	Asn	Asp	Lys	Ile	Trp	Val	Gly	Tyr	Asp	Asp	Leu	
				325					330					335		
gcc	agt	ata	tca	tgc	aag	ttg	gct	ttc	ctg	aaa	gaa	tta	ggc	gtt	tct	1056
Ala	Ser	Ile	Ser	Cys	Lys	Leu	Ala	Phe	Leu	Lys	Glu	Leu	Gly	Val	Ser	
			340					345					350			
ggt	gtc	atg	gtt	tgg	tca	ttg	gaa	aat	gat	gat	ttc	aaa	ggt	cac	tgc	1104
Gly	Val	Met	Val	Trp	Ser	Leu	Glu	Asn	Asp	Asp	Phe	Lys	Gly	His	Cys	
		355				360					365					
gga	ccg	aaa	aat	cca	ttg	ttg	aac	aaa	gtt	cat	aat	atg	att	aat	ggc	1152
Gly	Pro	Lys	Asn	Pro	Leu	Leu	Asn	Lys	Val	His	Asn	Met	Ile	Asn	Gly	
		370				375					380					
gat	gaa	aag	aac	tct	ttc	gaa	tgc	att	ttg	ggt	cca	agt	aca	acg	aca	1200

Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser Thr Thr Thr  
385 390 395 400

cca act cca acg acg aca ccc aca acc ccg act aca acg cca aca act 1248  
Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr Pro Thr Thr  
405 410 415

cct tct ccc acc acc ccg aca aca acc cct tct ccc acc acc ccg aca 1296  
Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr  
420 425 430

aca acc cct tct ccc acc aca ccg aca aca act cct tct ccc acc aca 1344  
Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr  
435 440 445

cca aca cca aca aca cca aca cca gcc cct aca aca tcg aca cct tcg 1392  
Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser Thr Pro Ser  
450 455 460

cca acc acg acc gaa cac aca agc gaa aca cca aaa tat aca acc tat 1440  
Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr  
465 470 475 480

gtc gat gga cat ctt atc aaa tgt tac aag gaa ggt gat atc cca cat 1488  
Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp Ile Pro His  
485 490 495

cca acc aat ata cac aaa tat ttg gtc tgt gaa ttt gtt aat ggt ggc 1536  
Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val Asn Gly Gly  
500 505 510

tgg tgg gtt cat att atg ccc tgt cca ccg ggc act att tgg tgt caa 1584  
Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile Trp Cys Gln  
515 520 525

gaa aaa ttg act tgt ata ggc gaa 1608  
Glu Lys Leu Thr Cys Ile Gly Glu  
530 535

<210> 21  
<211> 536  
<212> PRT  
<213> Dermatophagoides farinae

<400> 21  
Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro Met Arg Ile  
1 5 10 15



Ser Lys Leu Lys Leu Gly Asp Pro Ala Lys Gly Met Ser Pro Pro Gly  
 275 280 285

Phe Ile Ser Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu Leu Cys Gln  
 290 295 300

Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu Tyr Tyr Asn  
 305 310 315 320

Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu  
 325 330 335

Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser  
 340 345 350

Gly Val Met Val Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys  
 355 360 365

Gly Pro Lys Asn Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly  
 370 375 380

Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser Thr Thr Thr  
 385 390 395 400

Pro Thr Pro Thr Thr Thr Pro Thr Thr Pro Thr Thr Thr Pro Thr Thr  
 405 410 415

Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr  
 420 425 430

Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr  
 435 440 445

Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser Thr Pro Ser  
 450 455 460

Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr  
 465 470 475 480

Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp Ile Pro His  
 485 490 495

Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val Asn Gly Gly  
 500 505 510

Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile Trp Cys Gln  
 515 520 525

001160-000000

Glu Lys Leu Thr Cys Ile Gly Glu  
530 535

<210> 22  
<211> 1608  
<212> DNA  
<213> Dermatophagoides farinae

<400> 22  
ttcgctata caagtcaatt tttcttgaca ccaaatagtg cccggtggac agggcataat 60  
atgaaccac cagccacat taacaaattc acagaccaa ttttgtgta tattggttg 120  
atgtgggata tcaccttct tgtaacattt gataagatgt ccatcgacat aggttgata 180  
ttttggtgtt tcgcttgtgt gttcggtcgt ggttggcgaa ggtgtcgatg ttgtaggggc 240  
tggtgttggg gttgttggg ttggtgtggg gggagaagga gttgttgtcg gtgtggtggg 300  
agaaggggtt gttgtcgggg ttggtgggaga aggggttgtt gtcgggggtg tgggagaagg 360  
agttgttggc gttgtagtcg ggggttgtggg tgtcgtcgtt ggagttggtg tcgttgact 420  
tggacccaaa atgcattcga aagagttctt ttcacgcca ttaatcatat tatgaacttt 480  
gttcaacaat ggatttttcg gtccgcagtg acctttgaaa tcatcatttt ccaatgacca 540  
aaccatgaca ccagaaacgc ctaattcttt caggaaagcc aacttgcag atatactggc 600  
cagatcatcg taaccgaccc agattttatc attgtaacca tatggagcat tgtaatatc 660  
atcgatttgg atatgccatt cttctttttg aaacaattga cacaattcta tatatgagag 720  
gacaccttct tcaccagaaa tgaaacctgg gggcgacatg cctttggctg gatctccaag 780  
tttgagtttg cttcgatctt caatgtcca agcacggcca tagaatggaa caccattac 840  
caatttgtct ctggtggcac cattgttcaa ataatagtgc atggtgtagt tgacattgaa 900  
gtaagtgtgc aactcatcag tttcatctgg tcgtttatac aacggagcat tgtgaccgta 960  
aaagttttcc catccacgt ggtaatcata tgtcatgaca ttcaccaat cgaacaattt 1020  
gttcaattct ttgatatcat aagctcggtc gattttgtct ttacctggtg atactgcagc 1080  
agtcaacaag tagccatgag gttcaaaagc gtctttaagt tctctaacca aagccaaata 1140  
gttttgttta tcgattttcg ggttacccaa tcgagatcca ggatactccc aatccaaatc 1200  
tagaccgtcg aacttgatatt cttgcaaaaa gtccaaaact gattgtatga attggtgacg 1260  
atatgttggg tttgcagcca ttcggaata ttttccgag cttcataacc aaccaccaag 1320  
tgaaatcatg gtggttaatt ctggattctt caatcgcaag ttgttgaaac gttcataacc 1380  
acgtttttcc catgagttat gggtatcatc ttggttaagga tcgaaaactt gaattgtgta 1440  
tttgatttca tcaatttttag cgaaaccata cattaaatgt gtacacttga atggatcaat 1500  
atcttcgata gtgtatggat caactttatg atatacggac catgttccaa cataacaaac 1560  
aattctcatc ggatttttcg aataatcatt atgatctcgt ttgatgga 1608

<210> 23  
<211> 25  
<212> PRT  
<213> Dermatophagoides farinae

<220>  
<223> At location 1, Xaa = any amino acid

<400> 23

Xaa Leu Glu Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His His  
1 5 10 15

Arg Gln Gly Glu Gly Lys Met Asp Pro  
20 25

<210> 24

<211> 33

<212> PRT

<213> Dermatophagoides farinae

<220>

<223> At locations, 18, 28, 31 and 32, Xaa = any amino  
acid

<400> 24

Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro Met Met Ile  
1 5 10 15

Val Xaa Tyr Gly Gly Ser Ser Gly Tyr Gln Ser Xaa Lys Arg Xaa Xaa  
20 25 30

Thr

<210> 25

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<223> At location 24, n = a, c, t or g

<400> 25

aaacgtgatc ataaygatta ytcnaaraay c

31

<210> 26

<211> 31

<212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 26

aaacgtgatc ataaygatta yagyaaraay c

31

<210> 27

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<223> At locations 12 and 21, n = a, c, t or g

<400> 27

ccttcttcac cnacratcaa ncc

23

<210> 28

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<223> At locations 12 and 21, n = a, c, t or g

<400> 28

ccttcttcac cnacratgaa ncc

23

<210> 29

<211> 13

<212> PRT

<213> Dermatophagoides farinae

<400> 29

Gln Tyr Gly Val Thr Gln Ala Val Val Thr Gln Pro Ala  
 1 5 10

<210> 30  
 <211> 11  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 30  
 Asp Glu Leu Leu Met Lys Ser Gly Pro Gly Pro  
 1 5 10

<210> 31  
 <211> 24  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 31  
 Asp Met Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile  
 1 5 10 15

Ala Val Gly Gly Ser Thr Met Ser  
 20

<210> 32  
 <211> 21  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 32  
 Asp Ala Asn Glu Glu Ala Arg Ser Gln Leu Pro Glu Thr Ala Met Val  
 1 5 10 15

Leu Ile Lys Ser Gln  
 20

<210> 33  
 <211> 21  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 33  
 Gln Ser Arg Asp Arg Asn Asp Lys Pro Tyr Xaa Ile Val Lys Lys Lys  
 1 5 10 15

00460-EB22990

Lys Lys Ala Leu Asp

20

<210> 34

<211> 1621

<212> DNA

<213> Dermatophagoides farinae

<220>

<221> CDS

<222> (14)..(1540)

<400> 34

agaacttatg aaa atg aaa acg aca ttt gca ttg ttt tgt ata tgg gcc 49

Met Lys Thr Thr Phe Ala Leu Phe Cys Ile Trp Ala

1

5

10

tgc att ggc ttg atg aat gcg gcc act aaa cga gat cac aat aat tat 97

Cys Ile Gly Leu Met Asn Ala Ala Thr Lys Arg Asp His Asn Asn Tyr

15

20

25

tcg aaa aat cca atg cga atc gta tgt tat gtt gga aca tgg tcc gtt 145

Ser Lys Asn Pro Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val

30

35

40

tat cat aaa gtt gat cca tac aca att gaa gat att gat cct ttc aaa 193

Tyr His Lys Val Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys

45

50

55

60

tgt act cat ttg atg tat ggt ttt gct aaa atc gat gaa tac aaa tac 241

Cys Thr His Leu Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr

65

70

75

acc att caa gtt ttt gat cca ttt caa gat gat aac cat aac tca tgg 289

Thr Ile Gln Val Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp

80

85

90

gaa aaa cac ggg tat gaa cgt ttc aac aac ttg aga ttg aag aat cca 337

Glu Lys His Gly Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro

95

100

105

gaa ttg acc acc atg att tca ttg ggt ggt tgg tat gaa ggt tca gaa 385

Glu Leu Thr Thr Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu

110

115

120

aaa tat tcg gat atg gca gcc aat cca aca tat cgt cag caa ttt gtt 433

Lys Tyr Ser Asp Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val	
125 130 135 140	
caa tca gtt ttg gac ttt ttg caa gaa tac aaa ttc gat ggc cta gat	481
Gln Ser Val Leu Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp	
145 150 155	
ttg gat tgg gaa tat cct gga tca cgg tta ggc aat cct aaa atc gat	529
Leu Asp Trp Glu Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp	
160 165 170	
aaa caa aac tat tta aca tta gtt aga gaa ctt aaa gag gca ttt gaa	577
Lys Gln Asn Tyr Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu	
175 180 185	
cct ttc ggc tac ttg ttg act gcc gca gta tca ccc ggt aaa gat aaa	625
Pro Phe Gly Tyr Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys	
190 195 200	
att gac gta gct tat gag ctc aaa gaa ttg aac caa ttg ttc gat tgg	673
Ile Asp Val Ala Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp	
205 210 215 220	
atg aat gtc atg act tat gat tac cat ggc gga tgg gaa aat gtt ttc	721
Met Asn Val Met Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe	
225 230 235	
ggc cat aat gct ccg ttg tat aaa cga ccc gat gaa acg gat gaa ttg	769
Gly His Asn Ala Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu	
240 245 250	
cac act tac ttc aat gtc aac tac acc atg cac tat tat ttg aac aat	817
His Thr Tyr Phe Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn	
255 260 265	
ggc gct act cga gac aaa ctt gtt atg ggt gtt cca ttc tat ggt cgt	865
Gly Ala Thr Arg Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg	
270 275 280	
gct tgg agc atc gaa gat cga agc aaa gtc aaa ctt ggc gat ccg gcc	913
Ala Trp Ser Ile Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala	
285 290 295 300	
aaa ggc atg tct cct cct ggt ttt att act ggt gaa gaa ggt gtt ctc	961
Lys Gly Met Ser Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu	
305 310 315	
tca tac atc gaa ttg tgt cag tta ttc cag aaa gaa gaa tgg cat att	1009

Ser Tyr Ile Glu Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile	
320 325 330	
caa tac gat gaa tat tac aat gct cca tac gga tat aat gat aaa atc	1057
Gln Tyr Asp Glu Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile	
335 340 345	
tgg gtt ggt tac gat gat ctg gct agt ata tca tgc aag ttg gcc ttt	1105
Trp Val Gly Tyr Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe	
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ctc aaa gaa ttg ggc gtc tct ggc gtt atg ata tgg tca ttg gaa aac	1153
Leu Lys Glu Leu Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn	
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gat gat ttc aaa ggt cat tgc gga ccg aaa tat cca ttg ttg aac aaa	1201
Asp Asp Phe Lys Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys	
385 390 395	
gtt cac aat atg atc aat ggt gat gaa aag aac tct tac gaa tgt ctt	1249
Val His Asn Met Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu	
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ttg ggc cca agt aca acc aca cca aca cca acc acc ccg tca act act	1297
Leu Gly Pro Ser Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr	
415 420 425	
tcg act acc aca cca acg cct acc acc acc gat agc aca agc gaa aca	1345
Ser Thr Thr Thr Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr	
430 435 440	
cca aaa tac act acg tat att gat gga cat ttg att aaa tgc tat aaa	1393
Pro Lys Tyr Thr Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys	
445 450 455 460	
caa ggt tat ctt cca cat cca act gat gtt cat aaa tat tta gtt tgt	1441
Gln Gly Tyr Leu Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys	
465 470 475	
gaa tat att gcc aca cca aac ggt ggt tgg tgg gta cac att atg gat	1489
Glu Tyr Ile Ala Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp	
480 485 490	
tgt cca aaa gga act aga tgg cac gca aca tta aaa aat tgt att caa	1537
Cys Pro Lys Gly Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln	
495 500 505	
gaa tgatctgata tatttgtaac tgttttttgc taaatgaaat ttaaataaaa	1590

Glu

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1621

<210> 35

<211> 509

<212> PRT

<213> Dermatophagoides farinae

<400> 35

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20 25 30

Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val  
35 40 45

Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu  
50 55 60

Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val  
65 70 75 80

Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly  
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr  
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp  
115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu  
130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu  
145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr  
165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr  
180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala

001160-26229900

205

Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu

450

455

460

Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala  
465 470 475 480

Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly  
485 490 495

Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu  
500 505

&lt;210&gt; 36

&lt;211&gt; 1621

&lt;212&gt; DNA

&lt;213&gt; Dermatophagoides farinae

&lt;400&gt; 36

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 acaaactaaa tatttatgaa catcagttgg atgtggaaga taaccttggt tatagcattt 240  
 aatcaaagt ccataaatat acgtagtgtt ttttgggtgt tcgcttgtgc tatcggtggt 300  
 ggtaggcggt ggtgtggtag tcgaagtagt tgacgggggtg gttggtgttg gtgtggttgt 360  
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 aacaagtgtg tctcgagtag cgccattgtt caaataatag tgcattggtg agttgacatt 840  
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 tacgattcgc attggatttt tcgaataatt attgtgatct cgttttagtgg ccgcattcat 1560  
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 t 1621



[illegible][illegible][illegible]



Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr	
340 345 350	
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Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu	
355 360 365	
ggc gtc tct ggc gtt atg ata tgg tca ttg gaa aac gat gat ttc aaa	1152
Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys	
370 375 380	
ggc cat tgc gga ccg aaa tat cca ttg ttg aac aaa gtt cac aat atg	1200
Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met	
385 390 395 400	
atc aat ggt gat gaa aag aac tct tac gaa tgt ctt ttg ggc cca agt	1248
Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser	
405 410 415	
aca acc aca cca aca cca acc acc ccg tca act act tcg act acc aca	1296
Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr	
420 425 430	
cca acg cct acc acc acc gat agc aca agc gaa aca cca aaa tac act	1344
Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr	
435 440 445	
acg tat att gat gga cat ttg att aaa tgc tat aaa caa ggt tat ctt	1392
Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu	
450 455 460	
cca cat cca act gat gtt cat aaa tat tta gtt tgt gaa tat att gcc	1440
Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala	
465 470 475 480	
aca cca aac ggt ggt tgg tgg gta cac att atg gat tgt cca aaa gga	1488
Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly	
485 490 495	
act aga tgg cac gca aca tta aaa aat tgt att caa gaa	1527
Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu	
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<210> 38  
 <211> 509  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 38

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20 25 30

Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val  
35 40 45

Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu  
50 55 60

Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val  
65 70 75 80

Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly  
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr  
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp  
115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu  
130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu  
145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr  
165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr  
180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala  
195 200 205

Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met  
210 215 220

Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala  
225 230 235 240

Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe

00160-2629900

245

250

255

Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg  
260 265 270

Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile  
275 280 285

Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser  
290 295 300

Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu  
305 310 315 320

Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu  
325 330 335

Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr  
340 345 350

Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu  
355 360 365

Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys  
370 375 380

Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met  
385 390 395 400

Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser  
405 410 415

Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr  
420 425 430

Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr  
435 440 445

Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu  
450 455 460

Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala  
465 470 475 480

Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly  
485 490 495

Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu

<210> 39  
 <211> 1527  
 <212> DNA  
 <213> *Dermatophagoides farinae*

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 atcagttgga tgtggaagat aaccttgttt atagcattta atcaaatgtc catcaatata 180  
 cgtagtgtat tttggtgttt cgcttgTgct atcggTggTg gtaggcgttg gtgtggtagt 240  
 cgaagtagtt gacggggTgg ttggtgtTgg tgtggttgta cttgggcca aaagacattc 300  
 gtaagagttc ttttcatcac cattgatcat attgtgaact ttgttcaaca atggatattt 360  
 cggTccgcaa tgacctttga aatcatcgTt ttccaatgac catatcataa cgccagagac 420  
 gcccaattct ttgagaaagg ccaacttgca tgatatacta gccagatcat cgtaaccaac 480  
 ccagatttta tcattatata cgtatggagc attgtaatat tcatcgTatt gaatatgcca 540  
 ttcttctttc tggataaact gacacaattc gatgtatgag agaacacctt cttcaccagt 600  
 aataaaaacca ggaggagaca tgcctttggc cggatcgcca agtttgactt tgcttcgac 660  
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<210> 40  
 <211> 1470  
 <212> DNA  
 <213> *Dermatophagoides farinae*

<220>  
 <221> CDS  
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<400> 40



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195 200 205	
tac cat ggc gga tgg gaa aat gtt ttc ggc cat aat gct ccg ttg tat	672
Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala Pro Leu Tyr	
210 215 220	
aaa cga ccc gat gaa acg gat gaa ttg cac act tac ttc aat gtc aac	720
Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe Asn Val Asn	
225 230 235 240	
tac acc atg cac tat tat ttg aac aat ggc gct act cga gac aaa ctt	768
Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg Asp Lys Leu	
245 250 255	
gtt atg ggt gtt cca ttc tat ggt cgt gct tgg agc atc gaa gat cga	816
Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile Glu Asp Arg	
260 265 270	
agc aaa gtc aaa ctt ggc gat ccg gcc aaa ggc atg tct cct cct ggt	864
Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser Pro Pro Gly	
275 280 285	
ttt att act ggt gaa gaa ggt gtt ctc tca tac atc gaa ttg tgt cag	912
Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu Leu Cys Gln	
290 295 300	
tta ttc cag aaa gaa gaa tgg cat att caa tac gat gaa tat tac aat	960
Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu Tyr Tyr Asn	
305 310 315 320	
gct cca tac gga tat aat gat aaa atc tgg gtt ggt tac gat gat ctg	1008
Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu	
325 330 335	
gct agt ata tca tgc aag ttg gcc ttt ctc aaa gaa ttg ggc gtc tct	1056
Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser	
340 345 350	
ggc gtt atg ata tgg tca ttg gaa aac gat gat ttc aaa ggt cat tgc	1104
Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys	
355 360 365	
gga ccg aaa tat cca ttg ttg aac aaa gtt cac aat atg atc aat ggt	1152
Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly	
370 375 380	



gat gaa aag aac tct tac gaa tgt ctt ttg ggc cca agt aca acc aca 1200  
 Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser Thr Thr Thr  
 385 390 395 400

cca aca cca acc acc ccg tca act act tcg act acc aca cca acg cct 1248  
 Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr Pro Thr Pro  
 405 410 415

acc acc acc gat agc aca agc gaa aca cca aaa tac act acg tat att 1296  
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 420 425 430

gat gga cat ttg att aaa tgc tat aaa caa ggt tat ctt cca cat cca 1344  
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 435 440 445

act gat gtt cat aaa tat tta gtt tgt gaa tat att gcc aca cca aac 1392  
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 450 455 460

ggg ggt tgg tgg gta cac att atg gat tgt cca aaa gga act aga tgg 1440  
 Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly Thr Arg Trp  
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 His Ala Thr Leu Lys Asn Cys Ile Gln Glu  
 485 490

<210> 41  
 <211> 490  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 41  
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 20 25 30

Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu Met Tyr Gly  
 35 40 45

Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val Phe Asp Pro  
 50 55 60

Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly Tyr Glu Arg



325

330

335

Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser  
340 345 350

Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys  
355 360 365

Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly  
370 375 380

Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser Thr Thr Thr  
385 390 395 400

Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr Pro Thr Pro  
405 410 415

Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr Thr Tyr Ile  
420 425 430

Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu Pro His Pro  
435 440 445

Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala Thr Pro Asn  
450 455 460

Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly Thr Arg Trp  
465 470 475 480

His Ala Thr Leu Lys Asn Cys Ile Gln Glu  
485 490

&lt;210&gt; 42

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Dermatophagoides farinae

&lt;400&gt; 42

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cgtagtgtat tttggtgttt cgcttgtgct atcgggtggtg gtaggcgttg gtgtggtagt 240  
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gtaagagttc ttttcatcac cattgatcat attgtgaact ttgttcaaca atggatattt 360  
cgggtccgcaa tgacctttga aatcatcggt ttccaatgac catatcataa cgccagagac 420  
gccaattct ttgagaaagg ccaacttgca tgatatacta gccagatcat cgtaaccaac 480

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catatccgaa tatttttctg aaccttcata ccaaccacc aatgaaatca tgggtggta 1200
ttctggattc ttcaatctca agttgttgaa acgttcatac ccgtgttttt cccatgagtt 1260
atggttatca tcttgaaatg gatcaaaaac ttgaatgggtg tatttgattt catcgatttt 1320
agcaaaacca tacatcaaat gagtacattt gaaaggatca atatcttcaa ttgtgtatgg 1380
atcaacttta tgataaacgg accatgttcc aacataacat acgattcgca ttggattttt 1440
cgaataatta ttgtgatctc gtttagtggc 1470

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<210> 43
<211> 510
<212> DNA
<213> Dermatophagoides farinae

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<220>
<221> CDS
<222> (1)..(510)

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<400> 43
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Asp Met Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile
1 5 10 15

gcc gtc ggt ggt tcg act atg tcc gat caa ttt tcc aag act gca gcg 96
Ala Val Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala
20 25 30

gta gaa cat tat cgg gaa acg ttt gtt gtt agc aca gtt gat ctt atg 144
Val Glu His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met
35 40 45

act cgt tat ggt ttc gat ggt gtc atg att gat tgg tct ggc atg caa 192
Thr Arg Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln
50 55 60

gcc aaa gat agt gat aat ttc att aaa ttg ttg gac aaa ttc gac gaa 240
Ala Lys Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu
65 70 75 80

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Ile Ala Ser Tyr Asp Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val  
 100 105 110

Asp Phe Met Asn Val Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His  
 115 120 125

Thr Val Gly His Ala Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu  
 130 135 140

Ala Tyr His Lys Arg Gly Ala Pro Arg His Lys Met Val Met Ala Val  
 145 150 155 160

Pro Phe Tyr Ala Arg Thr Trp Ile Leu Glu  
 165 170

<210> 45  
 <211> 510  
 <212> DNA  
 <213> Dermatophagoides farinae

<400> 45  
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 gcctcgtttg tggtaagctt ctacggtttt gagttgttca ggaaacggag aagcatgacc 120  
 gaccgatg gcccatgac cagtgtaatc cagactaagc acgttcataa aatcgacata 180  
 gttggagatg gcaggaatgt tatagttatc gtatgatgcg atcgttgccg gcaaggtaac 240  
 acccatcaca aacgaggtgt gagcaaaactt ttcgtcgaat ttgtccaaca atttaatgaa 300  
 attatcacta tctttggctt gcatgccaga ccaatcaatc atgacaccat cgaaaccata 360  
 acgagtcata agatcaactg tgctaacaac aaacgtttcc cgataatgtt ctaccgctgc 420  
 agtcttgga aattgatcgg acatagtcga accaccgacg gcgatcatgg ctttggcggtt 480  
 gcccttatgt tgtgtaaaat gttccatata 510

<210> 46  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<220>  
 <223> At location 15, n = a, c t or g

<400> 46  
gaaccaaaaa chgtntgyta ytayg 25

<210> 47  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 47  
gtaaaacgac ggccagt 17

<210> 48  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 48  
gatatggaac atttyachca acayaargg 29

<210> 49  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 49  
gtaatacgac tcactatagg gc 22

<210> 50  
<211> 1445  
<212> DNA  
<213> Dermatophagoides farinae

[illegible]

<222> (14) .. (1399)

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Met Thr Arg Phe Ser Leu Thr Val Leu Ala Val Leu  
1 5 10

gcc gct tgt ttc ggt tca aat att cgt ccg aat gtg gca act ttg gaa 97  
Ala Ala Cys Phe Gly Ser Asn Ile Arg Pro Asn Val Ala Thr Leu Glu  
15 20 25

cct aaa act gta tgt tac tat gaa tct tgg gta cat tgg cgc caa ggt 145  
Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His Trp Arg Gln Gly  
30 35 40

gaa ggc aaa atg gat ccc gaa gac ata gat aca tcg ttg tgt act cac 193  
Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu Cys Thr His  
45 50 55 60

att gtc tac tct tat ttc ggc att gat gct gcc act cat gag att aaa 241  
Ile Val Tyr Ser Tyr Phe Gly Ile Asp Ala Ala Thr His Glu Ile Lys  
65 70 75

cta ttg gat gaa tat ctt atg aaa gat tta cat gac atg gaa cat ttc 289  
Leu Leu Asp Glu Tyr Leu Met Lys Asp Leu His Asp Met Glu His Phe  
80 85 90

acg cag cat aag ggc aac gcc aaa gcc atg atc gcc gtc ggt ggt tcg 337  
Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile Ala Val Gly Gly Ser  
95 100 105

act atg tcc gat caa ttt tcc aag act gca gcg gta gaa cat tat cgg 385  
Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala Val Glu His Tyr Arg  
110 115 120

gaa acg ttt gtt gtt agc aca gtt gat ctt atg act cgt tat ggt ttc 433  
Glu Thr Phe Val Val Ser Thr Val Asp Leu Met Thr Arg Tyr Gly Phe  
125 130 135 140

gat ggt gtc atg att gat tgg tct ggc atg caa gcc aaa gat agt gat 481  
Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln Ala Lys Asp Ser Asp  
145 150 155

aat ttc att aaa ttg ttg gac aaa ttc gac gaa aag ttt gct cac acc 529  
Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu Lys Phe Ala His Thr  
160 165 170



tcg ttt gtg atg ggt gtt acc ttg ccg gca acg atc gca tca tac gat	577
Ser Phe Val Met Gly Val Thr Leu Pro Ala Thr Ile Ala Ser Tyr Asp	
175 180 185	
aac tat aac att cct gcc atc tcc aac tat gtc gat ttt atg aac gtg	625
Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val Asp Phe Met Asn Val	
190 195 200	
ctt agt ctg gat tac act gga tca tgg gcc cat acg gtc ggt cat gct	673
Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His Thr Val Gly His Ala	
205 210 215 220	
tct ccg ttt cct gaa caa ctc aaa acg cta gaa gct tac cac aaa cga	721
Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu Ala Tyr His Lys Arg	
225 230 235	
ggc gct cca cgt cat aag atg gtc atg gct gta cca ttt tat gca cgt	769
Gly Ala Pro Arg His Lys Met Val Met Ala Val Pro Phe Tyr Ala Arg	
240 245 250	
acc tgg att ctc gag aaa atg aac aaa cag gac att ggc gat aaa gct	817
Thr Trp Ile Leu Glu Lys Met Asn Lys Gln Asp Ile Gly Asp Lys Ala	
255 260 265	
agt gga cca ggc cca cga ggt cag ttt aca cag act gat ggt ttc ctt	865
Ser Gly Pro Gly Pro Arg Gly Gln Phe Thr Gln Thr Asp Gly Phe Leu	
270 275 280	
agc tac aac gaa ttg tgc gtt cag att cag gcc gaa acg aat gca ttc	913
Ser Tyr Asn Glu Leu Cys Val Gln Ile Gln Ala Glu Thr Asn Ala Phe	
285 290 295 300	
acc att act cgt gat cat gat aat acc gca att tac gct gtc tat gtg	961
Thr Ile Thr Arg Asp His Asp Asn Thr Ala Ile Tyr Ala Val Tyr Val	
305 310 315	
cat agc aac cat gca gaa tgg atc tct ttc gaa gac cga cat aca ctt	1009
His Ser Asn His Ala Glu Trp Ile Ser Phe Glu Asp Arg His Thr Leu	
320 325 330	
ggc gaa aaa gca aaa aac ata acc caa caa gga tat gct gga atg tca	1057
Gly Glu Lys Ala Lys Asn Ile Thr Gln Gln Gly Tyr Ala Gly Met Ser	
335 340 345	
gtc tac aca ttg tcc aac gaa gat gtg cac ggc gtt tgt ggt gat aaa	1105
Val Tyr Thr Leu Ser Asn Glu Asp Val His Gly Val Cys Gly Asp Lys	
350 355 360	

aac cct ttg ttg cat gct atc caa tcg aac tat tat cat ggc gtg gta 1153  
 Asn Pro Leu Leu His Ala Ile Gln Ser Asn Tyr Tyr His Gly Val Val  
 365 370 375 380

acc gaa ccg acc gtc gtt aca ctt cct cca gtc aca cat aca aca gaa 1201  
 Thr Glu Pro Thr Val Val Thr Leu Pro Pro Val Thr His Thr Thr Glu  
 385 390 395

cat gtg acc gat ata cca ggc gtg ttt cat tgc cat gaa gaa gga ttc 1249  
 His Val Thr Asp Ile Pro Gly Val Phe His Cys His Glu Glu Gly Phe  
 400 405 410

ttc cgc gat aag acc tat tgt gcc aca tac tac gaa tgc aaa aaa ggc 1297  
 Phe Arg Asp Lys Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys Lys Lys Gly  
 415 420 425

gat ttt gga ctg gag aaa acc gtg cat cat tgt gcc aat cac tta cag 1345  
 Asp Phe Gly Leu Glu Lys Thr Val His His Cys Ala Asn His Leu Gln  
 430 435 440

gca ttt gac gaa gta agt cgg aca tgt att gat cat acc aaa ata ccc 1393  
 Ala Phe Asp Glu Val Ser Arg Thr Cys Ile Asp His Thr Lys Ile Pro  
 445 450 455 460

ggc tgt tgaatacaaa taaaattaca atcactttaaa aaaaaaaaaa aaaaaa 1445  
 Gly Cys

<210> 51  
 <211> 462  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 51  
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 20 25 30

Cys Tyr Tyr Glu Ser Trp Val His Trp Arg Gln Gly Glu Gly Lys Met  
 35 40 45

Asp Pro Glu Asp Ile Asp Thr Ser Leu Cys Thr His Ile Val Tyr Ser  
 50 55 60

Tyr Phe Gly Ile Asp Ala Ala Thr His Glu Ile Lys Leu Leu Asp Glu

80

95

110

125

140

160

175

190

205

220

240

255

270

285

300

320

Ala Glu Trp Ile Ser Phe Glu Asp Arg His Thr Leu Gly Glu Lys Ala

325

330

335

Lys Asn Ile Thr Gln Gln Gly Tyr Ala Gly Met Ser Val Tyr Thr Leu  
340 345 350

Ser Asn Glu Asp Val His Gly Val Cys Gly Asp Lys Asn Pro Leu Leu  
355 360 365

His Ala Ile Gln Ser Asn Tyr Tyr His Gly Val Val Thr Glu Pro Thr  
370 375 380

Val Val Thr Leu Pro Pro Val Thr His Thr Thr Glu His Val Thr Asp  
385 390 395 400

Ile Pro Gly Val Phe His Cys His Glu Glu Gly Phe Phe Arg Asp Lys  
405 410 415

Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys Lys Lys Gly Asp Phe Gly Leu  
420 425 430

Glu Lys Thr Val His His Cys Ala Asn His Leu Gln Ala Phe Asp Glu  
435 440 445

Val Ser Arg Thr Cys Ile Asp His Thr Lys Ile Pro Gly Cys  
450 455 460

<210> 52

<211> 1445

<212> DNA

<213> Dermatophagoides farinae

<400> 52

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gatgcacggg tttctccagt ccaaaatcgc cttttttgca ttcgtagtat gtggcacaat 180  
aggtcttata gcggaagaat ccttcttcat ggcaatgaaa cacgcctggg atatcgggtca 240  
catgttctgt tgtatgtgtg actggaggaa gtgtaacgac ggtcgggttcg gttaccacgc 300  
catgataata gttcgattgg atagcatgca acaaagggtt tttatcacca caaacgccgt 360  
gcacatcttc gttggacaat gtgtagactg acattccagc atatccttgt tgggttatgt 420  
tttttgcttt ttcaccaagt gtatgtcggg cttcgaaaga gatccattct gcatggttgc 480  
tatgcacata gacagcgtaa attgcggtat tatcatgata acgagtaatg gtgaatgcat 540  
tcgtttcggc ctgaatctga acgcacaatt cgttgtagct aaggaaacca tcagtctgtg 600  
taaactgacc tcgtgggcct ggtccactag ctttatcgcc aatgtcctgt ttgttcattt 660  
tctcgagaat ccaggtagct gcataaaatg gtacagccat gaccatctta tgacgtggag 720  
cgcctcgttt gtggtaagct tctagcgttt tgagttgttc aggaaacgga gaagcatgac 780  
cgaccgtatg ggcccatgat ccagtgtaat ccagactaag cacgttcata aaatcgacat 840

agttggagat ggcaggaatg ttatagttat cgtatgatgc gatcgttgcc ggcaaggtaa 900  
 caccatcac aaacgaggtg tgagcaaaact tttcgtcgaa tttgtccaac aatttaata 960  
 aattatcact atcttttggt tgcattgccag accaatcaat catgacacca tcgaaacat 1020  
 aacgagtcatt aagatcaact gtgctaacaa caaacgtttc ccgataatgt tctaccgctg 1080  
 cagtcttgga aaattgatcg gacatagtcg aaccaccgac ggcgatcatg gctttggcgt 1140  
 tgcccttatg ctgcgtgaaa tgttccatgt catgtaaatc tttcataaga tattcatcca 1200  
 atagtttaat ctcatgagtg gcagcatcaa tgccgaaata agagtagaca atgtgagtac 1260  
 acaacgatgt atctatgtct tcgggatcca ttttgcttc accttggcgc caatgtacc 1320  
 aagattcata gtaacatata gttttagggt ccaaagttgc cacattcgga cgaatatttg 1380  
 aaccgaaaca agcggcaagt acggccaata cagtcaaaga gaatcgagtc atttttat 1440  
 gggat 1445

<210> 53

<211> 1386

<212> DNA

<213> *Dermatophagoides farinae*

<400> 53

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 tggcgccaag gtgaaggcaa aatggatccc gaagacatag atacatcggt gtgtactcac 180  
 attgtctact cttatttcgg cattgatgct gccactcatg agattaaact attggatgaa 240  
 tatcttatga aagatttaca tgacatggaa catttcacgc agcataaggg caacgccaaa 300  
 gccatgatcg ccgtcgggtg ttcgactatg tccgatcaat tttccaagac tgcagcggta 360  
 gaacattatc gggaaacggt tgttgttagc acagttgatc ttatgactcg ttatggtttc 420  
 gatgggtgtc tgaattgatt gtctggcatg caagccaaag atagtataaa tttcattaaa 480  
 ttgttggaca aattcgacga aaagtgtgct cacacctcgt ttgtgatggg tgttaccttg 540  
 ccggcaacga tcgcatcata cgataactat aacattcctg ccatctcaa ctatgtcgat 600  
 tttatgaacg tgcttagtct ggattacact ggatcatggg ccatacggg cggatcatgct 660  
 tctccgtttc ctgaacaact caaaacgcta gaagcttacc acaaacgagg cgtccacgt 720  
 cataagatgg tcatggctgt accattttat gcacgtacct ggattctcga gaaaatgaac 780  
 aaacaggaca ttggcgataa agctagtggg ccaggccac gaggtcagtt tacacagact 840  
 gatgggttcc ttagctacaa cgaattgtgc gttcagattc aggccgaaac gaatgcattc 900  
 accattactc gtgatcatga taataccgca atttacgctg tctatgtgca tagcaaccat 960  
 gcagaatgga tctctttcga agaccgacat acacttggtg aaaaagcaaa aaacataacc 1020  
 caacaaggat atgctggaat gtcagtctac acattgtcca acgaagatgt gcacggcgtt 1080  
 tgtggtgata aaaacccttt gttgcatgct atccaatcga actattatca tggcgtggta 1140  
 accgaaccga ccgtcgttac acttcctcca gtcacacata caacagaaca tgtgaccgat 1200  
 ataccaggcg tgtttcattg ccatgaagaa ggattcttcc gcgataagac ctattgtgcc 1260  
 acatactacg aatgcaaaaa aggcgatttt ggactggaga aaaccgtgca tcattgtgcc 1320  
 aatcacttac aggcatttga cgaagtaagt cggacatgta ttgatcatac caaaataccc 1380  
 ggttgt 1386

<210> 54

<211> 1386

<212> DNA

<213> Dermatophagoides farinae

<400> 54

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gtatgtggca caataggtct tatcgcgga gaatccttct tcatggcaat gaaacacgcc 180  
tggatatatcg gtcacatggt ctggttgatg tgtgactgga ggaagtgtaa cgacggtcgg 240  
ttcggttacc acgccatgat aatagttcga ttggatagca tgcaacaaag ggttttttatc 300  
accacaaacg ccgtgcacat cttcgttgga caatgtgtag actgacattc cagcatatcc 360  
ttggttgggtt atgttttttg ctttttcacc aagtgtatgt cggctcttga aagagatcca 420  
ttctgcatgg ttgctatgca catagacagc gtaaattgcg gtattatcat gatcacgagt 480  
aatggtgaat gcattcgttt cggcctgaat ctgaacgcac aattcgttgt agctaaggaa 540  
accatcagtc tgtgtaaact gacctcgtgg gcctgggtcca ctagctttat cgccaatgtc 600  
ctggtttgttc attttctcga gaatccaggt acgtgcataa aatgggtacag ccatgaccat 660  
cttatgacgt ggagcgcctc gtttgtggta agcttctagc gttttgagtt gttcaggaaa 720  
cggagaagca tgaccgaccg tatgggcccata tgatccagtg taatccagac taagcacgtt 780  
cataaaatcg acatagtttg agatggcagg aatgttatag ttatcgtatg atgcgatcgt 840  
tgccggcaag gtaacaccca tcacaaacga ggtgtgagca aacttttctg cgaatttgtc 900  
caacaattta atgaaattat cactatcttt ggcttgcatt ccagaccaat caatcatgac 960  
accatcgaaa ccataacgag tcataagatc aactgtgcta acaacaaacg tttcccgata 1020  
atgttctacc gctgcagtct tggaaaattg atcggacata gtcgaaccac cgacggcgat 1080  
catggctttg gcgttgccct tatgctgcgt gaaatgttcc atgtcatgta aatctttcat 1140  
aagatattca tccaatagtt taatctcatg agtggcagca tcaatgccga aataagagta 1200  
gacaatgtga gtacacaacg atgtatctat gtcttcggga tccattttgc cttcaccttg 1260  
gcgccaatgt acccaagatt catagtaaca tacagtttta gggtccaaag ttgccacatt 1320  
cggacgaata tttgaaccga aacaagcggc aagtacggcc aatacagtca aagagaatcg 1380  
agtcatt 1386

<210> 55

<211> 1236

<212> DNA

<213> Dermatophagoides farinae

<220>

<221> CDS

<222> (1)..(1236)

<400> 55

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Thr Leu Glu Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His Trp  
1 5 10 15  
  
cgc caa ggt gaa ggc aaa atg gat ccc gaa gac ata gat aca tcg ttg 96  
Arg Gln Gly Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu  
20 25 30  
  
tgt act cac att gtc tac tct tat ttc ggc att gat gct gcc act cat 144

Cys	Thr	His	Ile	Val	Tyr	Ser	Tyr	Phe	Gly	Ile	Asp	Ala	Ala	Thr	His	
		35					40					45				
gag	att	aaa	cta	ttg	gat	gaa	tat	ctt	atg	aaa	gat	tta	cat	gac	atg	192
Glu	Ile	Lys	Leu	Leu	Asp	Glu	Tyr	Leu	Met	Lys	Asp	Leu	His	Asp	Met	
	50					55				60						
gaa	cat	ttc	acg	cag	cat	aag	ggc	aac	gcc	aaa	gcc	atg	atc	gcc	gtc	240
Glu	His	Phe	Thr	Gln	His	Lys	Gly	Asn	Ala	Lys	Ala	Met	Ile	Ala	Val	
	65				70				75					80		
ggt	ggt	tcg	act	atg	tcc	gat	caa	ttt	tcc	aag	act	gca	gcg	gta	gaa	288
Gly	Gly	Ser	Thr	Met	Ser	Asp	Gln	Phe	Ser	Lys	Thr	Ala	Ala	Val	Glu	
				85				90						95		
cat	tat	cgg	gaa	acg	ttt	gtt	gtt	agc	aca	gtt	gat	ctt	atg	act	cgt	336
His	Tyr	Arg	Glu	Thr	Phe	Val	Val	Ser	Thr	Val	Asp	Leu	Met	Thr	Arg	
		100						105					110			
tat	ggt	ttc	gat	ggt	gtc	atg	att	gat	tgg	tct	ggc	atg	caa	gcc	aaa	384
Tyr	Gly	Phe	Asp	Gly	Val	Met	Ile	Asp	Trp	Ser	Gly	Met	Gln	Ala	Lys	
	115					120					125					
gat	agt	gat	aat	ttc	att	aaa	ttg	ttg	gac	aaa	ttc	gac	gaa	aag	ttt	432
Asp	Ser	Asp	Asn	Phe	Ile	Lys	Leu	Leu	Asp	Lys	Phe	Asp	Glu	Lys	Phe	
	130					135					140					
gct	cac	acc	tcg	ttt	gtg	atg	ggt	gtt	acc	ttg	ccg	gca	acg	atc	gca	480
Ala	His	Thr	Ser	Phe	Val	Met	Gly	Val	Thr	Leu	Pro	Ala	Thr	Ile	Ala	
	145				150					155				160		
tca	tac	gat	aac	tat	aac	att	cct	gcc	atc	tcc	aac	tat	gtc	gat	ttt	528
Ser	Tyr	Asp	Asn	Tyr	Asn	Ile	Pro	Ala	Ile	Ser	Asn	Tyr	Val	Asp	Phe	
			165					170					175			
atg	aac	gtg	ctt	agt	ctg	gat	tac	act	gga	tca	tgg	gcc	cat	acg	gtc	576
Met	Asn	Val	Leu	Ser	Leu	Asp	Tyr	Thr	Gly	Ser	Trp	Ala	His	Thr	Val	
		180						185					190			
ggt	cat	gct	tct	ccg	ttt	cct	gaa	caa	ctc	aaa	acg	cta	gaa	gct	tac	624
Gly	His	Ala	Ser	Pro	Phe	Pro	Glu	Gln	Leu	Lys	Thr	Leu	Glu	Ala	Tyr	
	195					200					205					
cac	aaa	cga	ggc	gct	cca	cgt	cat	aag	atg	gtc	atg	gct	gta	cca	ttt	672
His	Lys	Arg	Gly	Ala	Pro	Arg	His	Lys	Met	Val	Met	Ala	Val	Pro	Phe	
	210					215					220					
tat	gca	cgt	acc	tgg	att	ctc	gag	aaa	atg	aac	aaa	cag	gac	att	ggc	720





<210> 56  
 <211> 412  
 <212> PRT  
 <213> Dermatophagoides farinae

<400> 56  
 Thr Leu Glu Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His Trp  
 1 5 10 15  
 Arg Gln Gly Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu  
 20 25 30  
 Cys Thr His Ile Val Tyr Ser Tyr Phe Gly Ile Asp Ala Ala Thr His  
 35 40 45  
 Glu Ile Lys Leu Leu Asp Glu Tyr Leu Met Lys Asp Leu His Asp Met  
 50 55 60  
 Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile Ala Val  
 65 70 75 80  
 Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala Val Glu  
 85 90 95  
 His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met Thr Arg  
 100 105 110  
 Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln Ala Lys  
 115 120 125  
 Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu Lys Phe  
 130 135 140  
 Ala His Thr Ser Phe Val Met Gly Val Thr Leu Pro Ala Thr Ile Ala  
 145 150 155 160  
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Tyr Ala Arg Thr Trp Ile Leu Glu Lys Met Asn Lys Gln Asp Ile Gly  
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Gly Phe Leu Ser Tyr Asn Glu Leu Cys Val Gln Ile Gln Ala Glu Thr  
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Asn Ala Phe Thr Ile Thr Arg Asp His Asp Asn Thr Ala Ile Tyr Ala  
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Val Tyr Val His Ser Asn His Ala Glu Trp Ile Ser Phe Glu Asp Arg  
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His Thr Leu Gly Glu Lys Ala Lys Asn Ile Thr Gln Gln Gly Tyr Ala  
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Gly Met Ser Val Tyr Thr Leu Ser Asn Glu Asp Val His Gly Val Cys  
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Gly Val Val Thr Glu Pro Thr Val Val Thr Leu Pro Pro Val Thr His  
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Thr Thr Glu His Val Thr Asp Ile Pro Gly Val Phe His Cys His Glu  
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